Table S7. Map2 CRISPR Primer Design and Off Targets

Primer	Sequence
Map2 sgRNAF	**GAAATTAATACGACTCACTATAGG**ATGCCACGCTGGACCTGCTTGTTTTAGAGCTAGAAATAGC
sgRNA common	AAAAGCACCGACTCGGTGCCACTTTTTCAAGTTGATAACGGACTAGCCTTATTTTAACTTGCTATTTCTAGCTCTAAAAC
Cas9 Forward	**TATTACGACTCACTATAGG**GAGAATGGACTATAAGGACCACGAC
Cas9 Reverse	GCGAGCTCTAGGAATTCTTAC
Repair oligo	*T*G*TTTCTCTTCAACAGATTGACAGCCAAAAGTTGAACTTCAGAGAGCATGCAAAGGCCCGGGTAGATCACGGGGCTGAGATCATCACACAGGAGCCAAGCAGGTCCAGCGTGGCATCACCCCGACGA*C*T*C
MAP2 F1	TGAACAGGTGGGAAAGAGCT
MAP2 R1	TGTCCTTGTTGCGGATGGAA

All sequences are written in the 5’ to 3’ direction.
Underlined sequences mark gRNA sites.
Sequences in **bold** are T7 promoter.
Glu knockin codon sequences are marked in red text in repair oligo.
Phosphorothioate linkages are marked with * in repair oligo.

Table S7. Map2 CRISPR Primer Design and Off Targets

Offtarget Seq	Mismatch Count	Offtarget Score	Chrom	Locus Description
ATGCCACACAGGGCCTGCTTGGG	3	0.559006211	chr17	intron:Kdm4b
ATGCCACACTAGACCAGCTATGG	4	0.511363636	chr18	intergenic:Zeb1-Arhgap12
GTGAGACACTGGACCTGCTTGGG	4	0.505263158	chr14	intergenic:Lmo7-Gm22347
AGGCCTTGCTGGACCTGCTTTGG	3	0.4875	chr15	intergenic:Rims2-Dcstamp
CTGCCACTTTGGACCAGCTTTGG	4	0.426136364	chr19	intergenic:Slc22a30-Gm6425
CTGCCAAGCTAGACCTGCTAAGG	4	0.361607143	chr3	intron:Zfhx4
ATGCCACTGAGGACCTGCTTGGG	3	0.331632653	chr16	intergenic:Mrps6-Kcne2
CTGCCCTGCTGGACCTGCTTGGG	3	0.316558442	chr15	intron:Cacna1i
TTGCCACGCTGGAACAACTTGGG	4	0.296969697	chr1	intergenic:Wdr64-Exo1
ATGCCACTCAGCACCTGCTTTGG	3	0.283613445	chr7	intergenic:Glrx3-Gm25798